

## AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** Method for determining the susceptibility to antiviral drugs of HIV viruses in a biological sample comprising polynucleic acids, with said method comprising:
  - a) ~~{if need be,}~~ releasing, isolating or concentrating the polynucleic acids present in the sample;
  - b) ~~{if need be}~~ amplifying ~~{the relevant}~~ part of a protease gene of HIV comprising codons 82 and 84 from the polynucleic acids with at least one suitable primer pair;
  - c) hybridizing the polynucleic acids of step a) or b) with ~~{at least two probes specifically hybridizing to a target sequence of the HIV protease gene, codon 82/84}~~ probes having the sequence of SEQ ID NO:267 and SEQ ID NO:354, or probes having sequence complementary to SEQ ID NO:267 and SEQ ID NO:354 ~~{the complement of said probe};~~  
~~{wherein said probes are capable of simultaneously hybridizing to their respective targets under appropriate hybridization and wash conditions;}~~  
wherein said probes are immobilized on a solid support; and
  - d) inferring from the result of step c) whether or not a mutation giving rise to drug resistance is present in said target ~~{sequences}~~ sequence.
2. (Cancelled)
3. **(Currently Amended)** ~~{Method according to claim 1, further}~~ A method for determining the susceptibility to antiviral drugs of HIV viruses in a biological sample comprising polynucleic acids, with said method comprising:
  - a) releasing, isolating or concentrating the polynucleic acids present in the sample;
  - b) optionally, amplifying part of a protease gene of HIV comprising codons 82 and 84 with at least one suitable primer pair;
  - c) hybridizing the polynucleic acids of step a) or b) with probes having the sequence of SEQ ID NO:267 and SEQ ID NO:354, or probes having sequences complementary to SEQ ID NO:267 and SEQ ID NO:354;  
wherein said probes are immobilized on a solid support; and

- d) inferring from the result of step c) whether or not a mutation giving rise to drug resistance is present in said target sequence ~~[characterized in that said probes are chosen from the following list: SEQ ID NO: 228 to SEQ ID NO: 357, SEQ ID NO: 517 to SEQ ID NO: 519 or the complement of said probes].~~
4. **(Currently Amended)** Method according to claim [1] 3 further characterized in that said primer pair is chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.
5. **(Currently Amended)** ~~[Method according to]~~ The method of claim [1] 3 ~~[further characterized in that:]~~ wherein step b) comprises amplifying a fragment of the protease gene with at least one 5'-primer specifically hybridizing to a target sequence located at nucleotide position 210 to 260 of the coding portion of the protease gene, in combination with at least one suitable 3'-primer.
6. **(Currently Amended)** The method of claim [1] 3 ~~[further characterized in that:]~~ wherein step b) comprises amplifying a fragment of the protease gene with at least one 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to position 300 of the coding portion of the protease gene, in combination with at least one suitable 5'-primer.
7. **(Previously Presented)** Method according to claim 5, further characterized in that the 5'-primer is SEQ ID NO: 5 and the 3'- primer is one primer or a combination of primers chosen from the following primers: SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.
8. **(Previously Presented)** Method according to claim 6, further characterized in that the 5'-primer is one primer or a combination of primers chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504 and the 3'-primer is SEQ ID NO: 6.
- 9.-33. (Cancelled)

- 34. **(New)** The method according to claim 1 wherein said primer pair is chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.
35. **(New)** The method of claim 1 wherein step b) comprises amplifying a fragment of the protease gene with at least one 5'-primer specifically hybridizing to a target sequence located at nucleotide position 210 to 260 of the coding portion of the protease gene, in combination with at least one suitable 3'-primer.
36. **(New)** The method of claim 1 wherein step b) comprises amplifying a fragment of the protease gene with at least one 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to position 300, in combination with at least one suitable 5'-primer.
37. **(New)** The method of claim 1 wherein the target sequences for codon 82/84 are provided by SEQ ID NO: 228-357.--